

Appendix C



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1bsv  

DOI 10.2210/pdb1bsv/pdb

Rad - Derived Information

Title GDP-FUCOSE SYNTHETASE FROM ESCHERICHIA COLI COMPLEX WITH NADPH

Authors Somers, W.S., Stahl, M.L., Sullivan, F.X.

Primary Citation Somers, W.S., Stahl, M.L., Sullivan, F.X. (1998) GDP-fucose synthetase from Escherichia coli: structure of a unique member of the short-chain dehydrogenase/reductase family that catalyzes two distinct reactions at the same active site. *Structure* 6: 1601-1612  
[Abstract] 

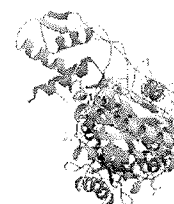
History Deposition 1998-08-31 Release 1999-08-26

Experimental Method Type X-RAY DIFFRACTION Data N/A

Parameters	Resolution[Å]	R-Value	R-Free	Space Group
	2.20	0.170 (obs.)	n/a	P 3 <sub>2</sub> 2 1
Unit Cell	Length [Å]	a	b	c
	Angles [°]	alpha	beta	gamma
		104.30	104.30	74.90
		90.00	90.00	120.00

To view the 3D structure  
click on one of the  
viewers under the image.

Images and Visualization

 Biological Molecule

Display Options



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\* Capable of displaying biological

Molecular Description Polymer 1 Molecule PROTEIN (GDP-FUCOSE SYNTHETASE) Chains A  
Asymmetric Unit


Classification Oxidoreductase

Source Polymer 1 Scientific Name Escherichia coli Common Name Bacteria Expression system Escherichia coli

Ligand Chemical Component	Identifier	Name	Formula	Drug Similarity	Hapten Similarity	Ligand Structure
NDP		NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE	C <sub>21</sub> H <sub>30</sub> N <sub>7</sub> O <sub>17</sub> P <sub>3</sub>			[ View ]

SCOP Classification (version 1.71)	Domain Info	Class	Fold	Superfamily	Family	Domain	Species
d1bsva_		Alpha and beta proteins (a/b)	NAD(P)-binding Rossmann-fold domains	NAD(P)-binding Rossmann-fold domains	Tyrosine-dependent oxidoreductases	GDP-4-keto-6-deoxy-d-mannose epimerase/reductase Esche (GDP-fucose synthetase)	

CATH Classification (version v3.1.0)	Domain	Class	Architecture	Topology	Homology
1bsvA01		Alpha Beta	3-Layer(aba) Sandwich	Rossmann fold	NAD(P)-bind Rossmann-li
1bsvA02		Alpha Beta	Alpha-Beta Complex	UDP-galactose 4-epimerase; domain 1	UDP-galacto epimerase, c

PFAM Classification	Chain	PFAM Accession	PFAM ID	Description	Type	Clan ID
A		PF01370 	Epimerase	NAD dependent epimerase/dehydratase family	Family	NADP_Rossm

GO Terms	Polymer	Molecular Function	Biological Process	Cellular Component
	PROTEIN (GDP-FUCOSE SYNTHETASE) (1BSV:A)	<ul style="list-style-type: none"><li>• catalytic activity</li><li>• coenzyme binding</li></ul>	<ul style="list-style-type: none"><li>• cellular metabolic process</li></ul>	<ul style="list-style-type: none"><li>• none</li></ul>

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